1600

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RAW SEQUENCE LISTING              DATE: 07/07/2003
PATENT APPLICATION:  US/09/692,077D    TIME: 08:49:53

Input Set : N:\Crf4\06272003\I692077.raw
Output Set: N:\CRF4\07072003\I692077D.raw
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 1 <110> APPLICANT: Liggett, Stephen
 2        Small, Kersten M.
 3 <120> TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
 4 <130> FILE REFERENCE: 10738-43
 5 <140> CURRENT APPLICATION NUMBER: US/09/692,077D
 6 <141> CURRENT FILING DATE: 2000-10-19
 7 <160> NUMBER OF SEQ ID NOS: 26
 8 <170> SOFTWARE: PatentIn version 3.2
10 <210> SEQ ID NO: 1
11 <211> LENGTH: 1353
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
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17        cgctcgctgc gcgcccctca gaacctgttc ctggtgtcgc tggccgccgc cgacatcctg     180
18        gtggccacgc tcatcatccc tttctcgctg gccaacgagc tgctgggcta ctggtacttc     240
19        cggcgcacgt ggtgcgaggt gtacctggcg ctcgacgtgc tcttctgcac ctcgtccatc     300
20        gtgcacctgt gcgccatcag cctggaccgc tactgggccg tgagccgcgc gctggagtac     360
21        aactccaagc gcaccccgcg ccgcatcaag tgcatcatcc tcactgtgtg gctcatcgcc     420
22        gccgtcatct cgctgccgcc cctcatctac aagggcgacc agggccccca gccgcgcggg     480
23        cgcccccagt gcaagctcaa ccaggaggcc tggtacatcc tggcctccag catcggatct     540
24        ttctttgctc cttgcctcat catgatcctt gtctacctgc gcatctacct gatcgccaaa     600
25        cgcagcaacc gcagaggtcc cagggccaag ggggggcctg ggcagggtga gtccaagcag     660
26        ccccgacccg accatggtgg ggctttggcc tcagccaaac tgccagccct ggcctctgtg     720
27        gcttctgcca gagaggtcaa cggacactcg aagtccactg gggagaagga ggaggggag     780
28        acccctgaag atactgggac ccgggccttg ccacccagtt gggctgccct tcccaactca     840
29        ggccagggcc agaaggaggg tgtttgtggg gcatctccag aggatgaagc tgaagaggag     900
30        gaagaggagg aggaggagga ggaagagtgt gaaccccagg cagtgccagt gtctccggcc     960
31        tcagcttgca gcccccccgct gcagcagcca caggggctccc gggtgctggc caccctacgt    1020
32        ggccaggtgc tcctgggcag gggcgtgggt gctataggtg ggcagtggtg gcgtcgaagg    1080
33        gcgcagctga cccgggagaa gcgcttcacc ttcgtgctgg ctgtggtcat ggcgtttttt    1140
34        gtgctctgct ggttcccctt cttcttcagc tacagcctgg cgccatctg cccgaagcac    1200
35        tgcaaggtgc cccatggcct cttccagttc ttcttctgga tcggctactg caacagctca    1260
36        ctgaaccctg ttatctacac catcttcaac caggacttcc gccgtgcctt ccggaggatc    1320
37        ctgtgccgcc cgtggaccca gacggcctgg tga                                   1353
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44        atggaccacc aggaccccta ctccgtgcag gccacagcgg ccatagcggc ggccatcacc      60
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46        cgctcgctgc gcgcccctca gaacctgttc ctggtgtcgc tggccgccgc cgacatcctg        180
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48        cggcgcacgt ggtgcgaggt gtacctggcg ctcgacgtgc tcttctgcac ctcgtccatc        300
49        gtgcacctgt gcgccatcag cctggaccgc tactgggccg tgagccgcgc gctggagtac        360
50        aactccaagc gcaccccgcg ccgcatcaag tgcatcatcc tcactgtgtg gctcatcgcc        420
51        gccgtcatct cgctgccgcc cctcatctac aagggcgacc agggcccccca gccgcgcggg        480
52        cgcccccagt gcaagctcaa ccaggaggcc tggtacatcc tggcctccag catcggatct        540
53        ttctttgctc cttgcctcat catgatcctt gtctacctgc gcatctacct gatcgccaaa        600
54        cgcagcaacc gcagaggtcc cagggccaag ggggggcctg ggcagggtga gtccaagcag        660
55        ccccgacccg accatggtgg ggctttggcc tcagccaaac tgccagccct ggcctctgtg        720
56        gcttctgcca gagaggtcaa cggacactcg aagtccactg gggagaagga ggaggggggag       780
57        acccctgaag atactgggac ccgggccttg ccacccagtt gggctgccct tcccaactca        840
58        ggccagggcc agaaggaggg tgtttgtggg gcatctccag aggatgaagc tgaagaggag        900
59        gaggaggagg aggaagagtg tgaaccccag gcagtgccag tgtctccggc ctcagcttgc        960
60        agcccccgc tgcagcagcc acagggctcc cgggtgctgg ccaccctacg tggccaggtg        1020
61        ctcctgggca ggggcgtggg tgctataggt gggcagtggt ggcgtcgaag ggcgcagctg        1080
62        acccgggaga agcgcttcac cttcgtgctg gctgtggtca ttggcgtttt tgtgctctgc        1140
63        tggttcccct tcttcttcag ctacagcctg ggcgccatct gcccgaagca ctgcaaggtg        1200
64        ccccatggcc tcttccagtt cttcttctgg atcggctact gcaacagctc actgaaccct        1260
65        gttatctaca ccatcttcaa ccaggacttc cgccgtgcct tccggaggat cctgtgccgc        1320
66        ccgtggaccc agacggcctg gtga                                               1344
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69 <211> LENGTH: 9
70 <212> TYPE: DNA
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76 <211> LENGTH: 9
77 <212> TYPE: DNA
78 <213> ORGANISM: Homo sapiens
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83 <211> LENGTH: 9
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85 <213> ORGANISM: Homo sapiens
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90 <211> LENGTH: 9
91 <212> TYPE: DNA
92 <213> ORGANISM: Homo sapiens
93 <400> SEQUENCE: 6
94        ctcctcctc                                                                9
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 450
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
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103     Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
104             20                  25                  30
105     Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
106             35                  40                  45
107     Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
108         50                  55                  60
109     Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
110     65                  70                  75                  80
111     Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
112                 85                  90                  95
113     Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
114                 100                 105                 110
115     Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
116             115                 120                 125
117     Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
118             130                 135                 140
119     Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
120     145                 150                 155                 160
121     Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
122                 165                 170                 175
123     Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
124                 180                 185                 190
125     Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
126                 195                 200                 205
127     Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
128             210                 215                 220
129     His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
130     225                 230                 235                 240
131     Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
132                 245                 250                 255
133     Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
134                 260                 265                 270
135     Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
136             275                 280                 285
137     Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
138             290                 295                 300
139     Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
140     305                 310                 315                 320
141     Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
142                 325                 330                 335
143     Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
144             340                 345                 350
145     Gly Gly Gln Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg
146             355                 360                 365
147     Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
148         370                 375                 380
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149        Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
150        385             390                 395                 400
151        Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
152                    405                 410                 415
153        Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
154                    420                 425                 430
155        Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
156                    435                 440                 445
157        Ala Trp
158                    450
160 <210> SEQ ID NO: 8
161 <211> LENGTH: 447
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 8
165        Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
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167        Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
168                    20                  25                  30
169        Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
170                    35                  40                  45
171        Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
172                50                  55                  60
173        Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
174        65                  70                  75                  80
175        Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
176                    85                  90                  95
177        Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
178                    100                 105                 110
179        Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
180                    115                 120                 125
181        Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
182                    130                 135                 140
183        Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
184        145                 150                 155                 160
185        Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
186                    165                 170                 175
187        Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
188                    180                 185                 190
189        Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
190                    195                 200                 205
191        Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
192                    210                 215                 220
193        His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
194        225                 230                 235                 240
195        Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
196                    245                 250                 255
197        Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
198                    260                 265                 270
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199        Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
200                275                 280                 285
201        Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
202                290                 295                 300
203        Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
204        305                 310                 315                 320
205        Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
206                325                 330                 335
207        Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
208                340                 345                 350
209        Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg Phe Thr Phe
210                355                 360                 365
211        Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
212                370                 375                 380
213        Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
214        385                 390                 395                 400
215        Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
216                405                 410                 415
217        Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
218                420                 425                 430
219        Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
220                435                 440                 445
222  <210> SEQ ID NO: 9
223  <211> LENGTH: 16
224  <212> TYPE: PRT
225  <213> ORGANISM: Homo sapiens
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232  <212> TYPE: PRT
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235        Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu
236        1                 5                 10
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239  <211> LENGTH: 3
240  <212> TYPE: PRT
241  <213> ORGANISM: Homo sapiens
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243        Glu Glu Glu
244        1
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247  <211> LENGTH: 3
248  <212> TYPE: PRT
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VERIFICATION SUMMARY   DATE: 07/07/2003
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Input Set : **N:\Crf4\06272003\I692077.raw**
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